modules individually and respectively selected from the group consisting of A, A′, a, and a′, said A module comprising SEQ ID No. 48, said A′ module comprising SEQ ID No. 52, said a module comprising SEQ ID No. 50, and said a′ module comprising SEQ ID No. 53; and

b. contacting said peptide with said first surface of said epithelial cell, and causing said peptide to alter the flux of water across said cell surface.

50. The method of claim 49, said plurality of polar amino acid residues including at least one lysine residue.

51. The method of claim 49, said plurality of polar amino acid residues comprising up to four lysine residues.

52. The method of claim 49, said peptide having from about 22-27 amino acid residues.

53. The method of claim 49, said peptide being substantially monomeric in solution.

54. The method of claim 49, said peptide being soluble to a level of at least about 5 mM.

55. The method of claim 49, said peptide being soluble to a level of at least about 10 mM.

56. The method of claim 49, said peptide having at least about 50% helical content.

57. The method of claim 49, said peptide having an activity profile of greater than about 15.0 $\mu A/cm^2$ in MDCK cells when applied to the MDCK cells at a concentration of about 500μM.

58. The method of claim 49, said peptide being selected from the group consisting of SEQ ID Nos. 9, 18, 19, 21, 26, 27, and 28.

59. The method of claim 49, said peptide including at least one amino acid residue positioned between said modules.

60. The method of claim 59, said at least one amino acid residue positioned between said modules being selected from the group consisting of alanine, lysine, and tryptophan.

61. A peptide having a total of from about 16-31 amino acid residues and comprising a plurality of polar amino acid residues at either the N- or C- terminus of said peptide

and at least two modules individually and respectively selected from the group consisting of A, A′, a, and a′, said A module comprising SEQ ID No. 48, said A′ module comprising SEQ ID No. 52, said a module comprising SEQ ID No. 50, and said a′ module comprising SEQ ID No. 53.

62. The peptide of claim 61, said plurality of polar amino acid residues including at least one lysine residue.

63. The peptide of claim 61, said plurality of polar amino acid residues comprising up to four lysine residues.

64. The peptide of claim 61, said peptide having from about 22-27 amino acid residues.

65. The peptide of claim 61, said peptide being substantially monomeric in solution.

66. The peptide of claim 61, said peptide being soluble to a level of at least about 5 mM.

67. The peptide of claim 61, said peptide being soluble to a level of at least about 10 mM.

68. The peptide of claim 61, said peptide having at least about 50% helical content.

69. The peptide of claim 61, said peptide having an activity profile of greater than about 15.0 $\mu A/cm^2$ in MDCK cells when applied to the MDCK cells at a concentration of about 500μM.

70. The peptide of claim 61, said peptide being selected from the group consisting of SEQ ID Nos. 9, 18, 19, 21, 26, 27, and 28.

71. The peptide of claim 61, said peptide including at least one amino acid residue positioned between said modules.

72. The peptide of claim 61, said at least one amino acid residue positioned between said modules being selected from the group consisting of alanine, lysine, and tryptophan